

MAY 08 2002

TECH CENTER 1600 2900



1600

RAW SEQUENCE LISTING

DATE: 05/01/2002

PATENT APPLICATION: US/09/234,733A

TIME: 13:06:29

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\05012002\I234733A.raw

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3 <110> APPLICANT: JIANG, Min
4     POTTER, Andrew A.
5     MACLACHLAN, Philip R.
7 <120> TITLE OF INVENTION: CAMP FACTOR OF STREPTOCOCCUS UBERIS
9 <130> FILE REFERENCE: 9000-0030.10
11 <140> CURRENT APPLICATION NUMBER: 09/234,733A
12 <141> CURRENT FILING DATE: 1999-01-21
14 <160> NUMBER OF SEQ ID NOS: 5
16 <170> SOFTWARE: PatentIn Ver. 2.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1191
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Description of Artificial Sequence: S. uberis CAMP
25     factor gene
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (157)..(924)
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32 aatgaacata aaataaaaat taataattat atatttttat gataatcaca tatatttgac 60
34 ttaaaaaaat tgttactgta tgatacaggc ataagtactt atttatttta tagattgcaa 120
36 tttataaaca atttatatttt tcaaagagga atgctt atq gaa ttc aaa aag tta 174
37                                     Met Glu Phe Lys Lys Leu
38                                     1           5
40 ctt tat tta act ggt tca atc gca gga att act tta ttt tcc cca att 222
41 leu tyr leu thr gly ser ile ala gly ile thr leu phe ser pro ile
42             10             15             20
44 tta aca agt gtc caa gca aat caa ata aat gtt agt caa cca tet aat 280
45 leu thr ser val gln ala asn gln ile asn val ser gln pro ser asn
46             25             30             35
48 aat gaa agt aat gtt att tca cag aaa aaa gaa gaa att gat aat agt 318
49 asn glu ser asn val ile ser gln lys lys glu glu ile asp asn ser
50             40             45             50
52 cta aat cag gaa agt gct caa cta tat gcc ttg aaa gaa gat gtt aaa 366
53 leu asn gln glu ser ala gln leu tyr ala leu lys glu asp val lys
54             55             60             65             70

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64 aat tcc att gga aca aga gta gaa gca atc tct gac gtg att caa gca 510
65 Asn Ser Ile Gly Thr Arg Val Glu Ala Ile Ser Asp Val Ile Gln Ala
66      105      110      115
68 att gtt ttt tca acg caa cag tta aca aat aaa gtt gat caa gct cac 558
69 Ile Val Phe Ser Thr Gln Gln Leu Thr Asn Lys Val Asp Gln Ala His
70      120      125      130
72 att gat atg gga ttt gct att acg aaa tta ctt att cgc att gca gac 606
73 Ile Asp Met Gly Phe Ala Ile Thr Lys Leu Leu Ile Arg Ile Ala Asp
74 135      140      145      150
76 cca ttt gct tca aat gaa tcc att aaa ggg caa gtc gaa gct gtt aaa 654
77 Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly Gln Val Glu Ala Val Lys
78      155      160      165
80 caa gtg caa gag act gtg ctt acc tat ccc gat ttg cag cct acg gat 702
81 Gln Val Gln Ala Thr Val Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp
82      170      175      180
84 aga gca act att tac gtt aaa tca aaa tta gac aag ctt att tgg caa 750
85 Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln
86      185      190      195
88 aca aga att acc aga gat caa aaa gtt ctt aat gta aag agt ttt gaa 798
89 Thr Arg Ile Thr Arg Asp Gln Lys Val Leu Asn Val Lys Ser Phe Glu
90      200      205      210
92 gtt tat cat caa tta aat aaa gct atc aca cat gca gta ggt gta caa 846
93 Val Tyr His Gln Leu Asn Lys Ala Ile Thr His Ala Val Gly Val Gln
94 215      220      225      230
96 tta aat cca act gta aca gtt gca caa gtt gac caa gaa atc aaa gtg 894
97 Leu Asn Pro Thr Val Thr Val Ala Gln Val Asp Gln Glu Ile Lys Val
98      235      240      245
100 cta caa gaa gca tta aat act gct cta cag taaggtagag attgaattga 944
101 Leu Gln Glu Ala Leu Asn Thr Ala Leu Gln
102      250      255
104 cgtattaaaa aggactggaa ttatttaatt tcagtccttt agaattttta tttagctgat 1004
106 ttacttggtg aagagatttg gtggaaaate aagtaccata cttcatttct cctccaaata 1064
108 cttgtatgtc gattcccttc taaaacatag ctaattagtt tagttttctg gctaatagat 1124
110 tgtacatgaa attgttcaaa attactaggg taaaagggtt ttctttttat aaattcatca 1184
112 tgaactat 1191
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116 <211> LENGTH: 256
117 <212> TYPE: PR1
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE
121 <223> OTHER INFORMATION Description of Artificial Sequence. CAMP factor
122      preprotein
124 <400> SEQUENCE: 2
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126      1      5      10      15
128 Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala Asn Gln Ile Asn

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134 Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala
135      50                      55                      60
137 Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser
138  65                      70                      75                      80
140 Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro
141      85                      90                      95
143 Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg Val Glu Ala Ile
144      100                     105                     110
146 Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn
147      115                     120                     125
149 Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu
150      130                     135                     140
152 Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly
153 145                      150                      155                      160
155 Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro
156      165                     170                     175
158 Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu
159      180                     185                     190
161 Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu
162      195                     200                     205
164 Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr
165      210                     215                     220
167 His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val
168 225                      230                      235                      240
170 Asp Gln Glu Ile Lys Val Leu Gln Glu Ala Leu Asn Thr Ala Leu Gln
171      245                     250                     255
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 256
176 <212> TYPE: PRT
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Description of Artificial Sequence: deduced S. uberis
181      CAMP factor protein
183 <400> SEQUENCE: 3
184 Met Glu Phe Lys Lys Leu Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile
185  1                      5                      10                      15
187 Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala Asn Gln Ile Asn
188      20                      25                      30
190 Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys
191      35                      40                      45
193 Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala
194      50                      55                      60
196 Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser
197  65                      70                      75                      80
199 Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro
200      85                      90                      95

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206          115          120          125
208 Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu
209          130          135          140
211 Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly
212 145          150          155          160
214 Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro
215          165          170          175
217 Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu
218          180          185          190
220 Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu
221          195          200          205
223 Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr
224          210          215          220
226 His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val
227 225          230          235          240
229 Asp Gln Glu Ile Lys Val Leu Gln Glu Ala Leu Asn Thr Ala Leu Gln
230          245          250          255
236 <210> SEQ ID NO: 4
237 <211> LENGTH: 226
238 <212> TYPE: PRT
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Description of Artificial Sequence: S. agalactiae
243 CAMP factor protein
245 <400> SEQUENCE: 4
246 Asp Gln Val Thr Thr Pro Gln Val Val Asn His Val Asn Ser Asn Asn
247 1 5 10 15
249 Gln Ala Gln Gln Met Ala Gln Lys Leu Asp Gln Asp Ser Ile Gln Leu
250 20 25 30
252 Arg Asn Ile Lys Asp Asn Val Gln Gly Thr Asp Tyr Glu Lys Pro Val
253 35 40 45
255 Asn Glu Ala Ile Thr Ser Val Glu Lys Leu Lys Thr Ser Leu Arg Ala
256 50 55 60
258 Asn Ser Glu Thr Val Tyr Asp Leu Asn Ser Ile Gly Ser Arg Val Glu
259 65 70 75 80
261 Ala Leu Thr Asp Val Ile Glu Ala Ile Thr Phe Ser Thr Gln His Leu
262 85 90 95
264 Ala Asn Lys Val Ser Gln Ala Asn Ile Asp Met Glu Phe Gly Ile Thr
265 100 105 110
267 Lys Leu Val Ile Arg Ile Leu Asp Pro Phe Ala Ser Val Asp Ser Ile
268 115 120 125
270 Lys Ala Gln Val Asn Asp Val Lys Ala Leu Glu Gln Lys Val Leu Thr
271 130 135 140
273 Tyr Pro Asp Leu Lys Pro Thr Asp Arg Ala Thr Ile Tyr Thr Lys Ser
274 145 150 155 160
276 Lys Leu Asp Lys Glu Ile Lys Asp Thr Arg Phe Thr Arg Asp Lys Lys

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282 Ile Thr His Ala Val Gly Val Gln Leu Asn Pro Asn Val Thr Val Gln
283      195      200      205
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288 Leu Lys
289 225
292 <210> SEQ ID NO: 5
293 <211> LENGTH: 228
294 <212> TYPE: PRT
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: Description of Artificial Sequence: mature S. uberis
299      CAMP factor protein
301 <400> SEQUENCE: 5
302 Asn Gln Ile Asn Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile
303      1      5      10      15
305 Ser Gln Lys Lys Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala
306      20      25      30
308 Gln Leu Tyr Ala Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln
309      35      40      45
311 Ser Val Asn Ser Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu
312      50      55      60
314 Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg
315      65      70      75      80
317 Val Glu Ala Ile Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln
318      85      90      95
320 Gln Leu Thr Asn Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala
321      100     105     110
323 Ile Thr Lys Leu Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu
324      115     120     125
326 Ser Ile Lys Gly Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val
327      130     135     140
329 Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val
330      145     150     155     160
332 Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp
333      165     170     175
335 Gln Lys Val Leu Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn
336      180     185     190
338 Lys Ala Ile Thr His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr
339      195     200     205
341 Val Ala Gln Val Asp Gln Glu Ile Lys Val Leu Gln Glu Ala Leu Asn
342      210     215     220
344 Thr Ala Leu Gln
345 225

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VERIFICATION SUMMARY

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